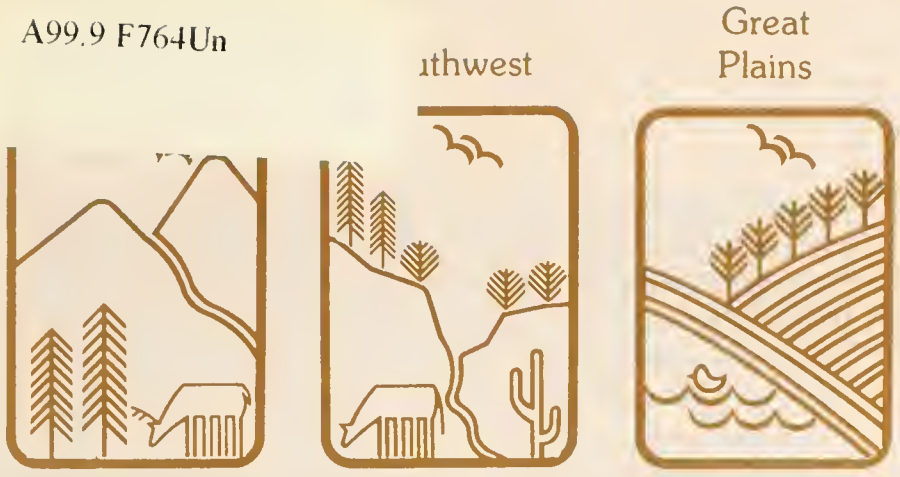
Historic, archived document

Do not assume content reflects current
scientific knowledge, policies, or practices.

A99.9 F764Un



Research Note RM-524

July 1993

USDA Forest Service
Rocky Mountain Forest and
Range Experiment Station

Modeling Initial Conditions for Root Rot in Forest Stands: Random Proportions

Michael A. Marsden, Bov B. Eav, and Matthew K. Thompson[1]

The Western Root Disease Model was developed to model *Armillaria* spp. and *Phellinus weirii* root disease in forest stands. This research note documents a refinement in the model. Modeling the initial conditions of root disease in a stand is more accurate with the use of generated random proportions for the degree of root system colonized by the disease. This is necessary to reflect the variation in the proportion of root systems colonized by the disease. A truncated-binomial distribution is used to generate the sequence of proportions for each sample tree. This technique may have application in the modeling of other forest pests.

Keywords: Simulation, truncated-binomial, pest modeling, root disease

Introduction

The Western Root Disease Model was developed to model the effects of *Armillaria* spp. and *Phellinus weirii* root diseases in forest stands (Stage et al. 1990). In modeling the dynamics of root disease it became necessary to deal with variables that are proportions (i.e., the proportion of the root system colonized on a live tree infected by root rots). A newly infected tree will have a small proportion of its root system colonized. A tree that has been infected for many years may have a substantial proportion of its root system colonized. The disease will colonize a larger proportion of the root system until the tree dies. The proportion of the root system colonized at the time of death is different for different tree species. In the root disease model when a tree is killed, *Armillaria* spp. will colonize the rest of the root system. *Phellinus weirii* is limited to the proportion of the root system colonized while the host tree is still alive. The proportion of the root system colonized can only be 1.00 for a tree killed by *Armillaria* spp. The proportion of the root system colonized for all other conditions depends on the tree species and whether it is infected with *Armillaria* spp. or *Phellinus weirii*.

The root disease model is linked to the Prognosis Model for Stand Development (Wykoff et al. 1982; Wykoff 1986). Stand inventory data from a variety of sampling designs can be used to set initial conditions for the simulation of the stand. Data on the status of the root disease may be taken as a separate inventory or as part of the timber inventory. In either case, the proportion of the root system colonized for an infected tree is assigned an average for the stand.

If the root disease conditions are recorded at time of stand inventory, infected trees are classified into broad classes with respect to disease conditions. The classes are: 1) trees located near infected trees (within 30 feet), 2) trees showing symptoms of infection, and 3) trees with crown deterioration. The model user must specify the average proportion of root system colonized for

[1] *Michael A. Marsden, Biometrician, Rocky Mountain Forest and Range Experiment Station, Fort Collins, Colorado; Bov B. Eav, Supervisory Operations Research Analyst, Forest Pest Management, Methods Application Group, Fort Collins, Colorado; Matthew K. Thompson, Computer Programmer, Senior Systems Analyst/Programmer, Management Assistance Corporation of America, Fort Collins, Colorado.*

infected trees in the stand. To distribute the proportion of root colonized to individual tree records, the following process was devised.

At the beginning of a simulation by the Western Root Disease Model, the user may accept a default value for the proportion of root colonized for infected trees (Stage et al. 1990). The default conditions are: 25 acres of a 100 acre stand are infected with root disease; 20 disease centers; 50 percent of the trees within a center are infected and, of these, the average proportion of root system colonized is 0.10. The user may override any of the default values by specifying another value. In all cases, the model then assigns a proportion of the root system colonized to each tree in a list of infected trees. Assigning each the same value does not result in realistic simulations. In the real system, some trees are infected for a longer time and have a greater proportion of their root system colonized than others (Kulhavy et al. 1984; Tkacz and Schmitz 1986). There is a distribution of proportions among the sample trees. Selecting values at random, from a range of permitted values based on the truncated-binomial distribution, is proposed to represent this variation in infected condition.

Tkacz and Schmitz (1986) reported the distribution of lodgepole pine trees infected by *Armillaria* spp. by class. The proportion of the tree's root system colonized by the disease was presented by classes: 0—no infection, 1—0.01-0.25, 2—0.26-0.50, 3—0.51-0.75, 4—0.76-1.00. We are not interested in the class with none of the root system colonized because this is covered by another parameter for the model. Of their 30 sample trees with infection, 9 were in class 1, 12 in class 2, 6 in class 3, and 3 in class 4 (fig. 1). To model this distribution, we chose the truncated-binomial distribution.

Pseudo-random number generators of the uniform distribution over the range 0 to 1 are often used in stochastic simulations. Good programs have been available for a number of years for the generation of uniform random numbers on 32 bit computers. The history of the development and the base procedure used in this study is described in STAT/LIBRARY TM by IMSL Inc., 1991. This distribution can be used to index any cumulative distribution to obtain a sequence of random numbers with the same distribution as that indexed. The proportions modeled here are expected to be clumped about their average. In young trees with expanding root systems, the proportion of the roots infected may remain low as root growth compensates for loss to infection. When the trees reach pole size, root expansion leads to contact with the root system of other trees and the possibility for transfer of infection, which in turn leads to an increase in the proportion of the root system colonized (Bloomberg and Reynolds 1985). At some point, tree mortality removes trees from the ranks of infected live trees and the proportion of root systems colonized reaches a second equilibrium.

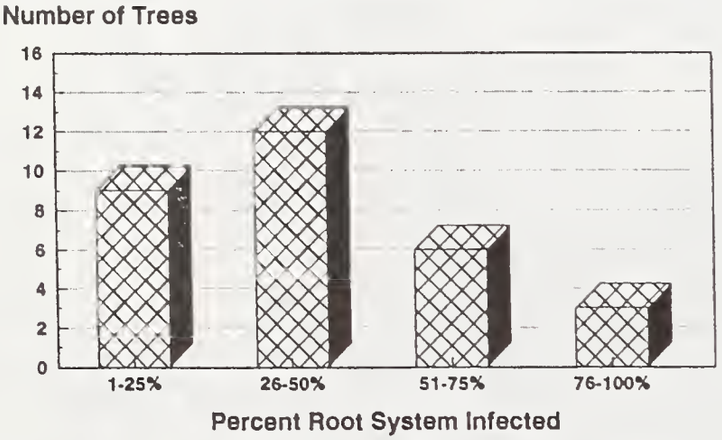


Figure 1.—The distribution of lodgepole pine trees by infection class (Tkacz and Schmitz 1986).

We devised the following scheme to draw a random proportion for each tree on the list. The uniform random number generator is used to locate an index into cumulative distribution for the truncated-binomial (Parzen 1967). The inverse of this value is the estimated proportion. The computer programs used in our model are presented in the Appendix.

Methods

The general binomial Probability Distribution Function, PDF, is written as:

$$PDF(x=k \mid P,N) = \frac{P^k(1-P)^{N-k}\, N!}{(N-k)!\; k!}$$

$$\text{for } k = 0,1,2,\ldots,N,\ 0 < P < 1\ ,$$

with a mean of NP and a variance of NP(1-P) (Parzen 1967).

Our application was to assign, at random, the proportion of root system colonized to each tree in a list of trees. For such cases, the probability of a zero value (no infection) is not included. For initial model conditions, the proportion of trees infected in a root disease center is set by another parameter. The probability of zero for the binomial distribution is:

$$PDF(x=0 \mid P,N) = (1-P)^N$$

This value is removed from the sequence of permitted values. The distribution function is then scaled so it sums to one over its new range. This gives us a truncated-binomial distribution of:

$$PDF(x=k \mid P,N) = \frac{P^k(1-P)^{N-k}\, N!}{(N-k)!\; k!\; (1-(1-P)^N)}$$

The expected value of this distribution with parameters P and N is different than that of the binomial distribution with the same parameters because we have eliminated the potential for a value of zero. While the

expected value of the binomial distribution is NP, the expected value for our truncated-binomial is NP/(1-(1-P)^N). The cumulative distribution function for our truncated-binomial is calculated the same as the binomial distribution using the PDF(.). Random values for a proportion are then selected using a random number drawn from the uniform distribution.

Consider the data from Tkacz and Schmitz (1986) where the proportions are in four equal classes: 0.01-0.25, 0.26-0.50, 0.51-0.75, and 0.76-1.00. The classes are equally spaced on the range of possible proportions. Here N = 4. If we multiply the class number by the class frequency, then divide by the total number of observations, we have a mean for this sample:

$$\text{mean} = (9 \times 1 + 12 \times 2 + 6 \times 3 + 3 \times 4)/(9 + 12 + 6 + 3) = 63/30 = 2.10$$

For the truncated-binomial distribution, the mean is NP/(1-(1-P^N)). So given N = 4, we can solve P. The first approximation is to let P = mean/N or 2.1/4 = 0.525, then substitute this value for P in the equation for the mean. When NP is divided by (1-(1-0.525)^4), we get 2.21, not 2.10, so our first estimate of P is a little high. By reducing P a small amount, we can compute the mean until we get as close to the value of 2.10 as we wish. P equal to 0.495 gives us an expected mean of 2.12, which is sufficient for this example. We can now compute the probability for each of the four classes and the cumulative probability, or the sum of the probabilities, of this class and all previous classes. This is done in table 1. To this we add a column for the expected cell frequency—the sample size (30) times the probability for each class. The observed and expected frequencies show close agreement (fig. 2). The next two columns in table 1 contain the observed frequency and the difference between the observed and expected frequency. The squared differences divided by the expected frequency is distributed as chi-square—as is the sum of these values. A chi-square computed value of 0.91 is less than the distribution value of 1.21 for 3 degrees of freedom and an alpha level of 0.75. This indicates that the data fit the truncated-binomial distribution extremely well.

If we accept the truncated-binomial distribution as a reasonable description of the expected distribution of

Table 1.—Truncated-binomial distribution where P = 0.495 and N = 4.

k	PDF(k)[1]	CDF(k)[2]	Expected frequency	Observed frequency	O-E
1	0.27	0.27	8.1	9	-0.9
2	0.40	0.67	12.0	12	0.0
3	0.26	0.93	7.8	6	1.8
4	0.07	1.00	2.1	3	9.0

Chi-square = (.9 × .9)/8.1 + (0 × 0)/12 + (1.8 × 1.8)/7.8 + (.9 × .9)/2.1 = 0.91

[1] PDF(k) is the value of the probability density function.
[2] CDF(k) is the value of the cumulative distribution function.

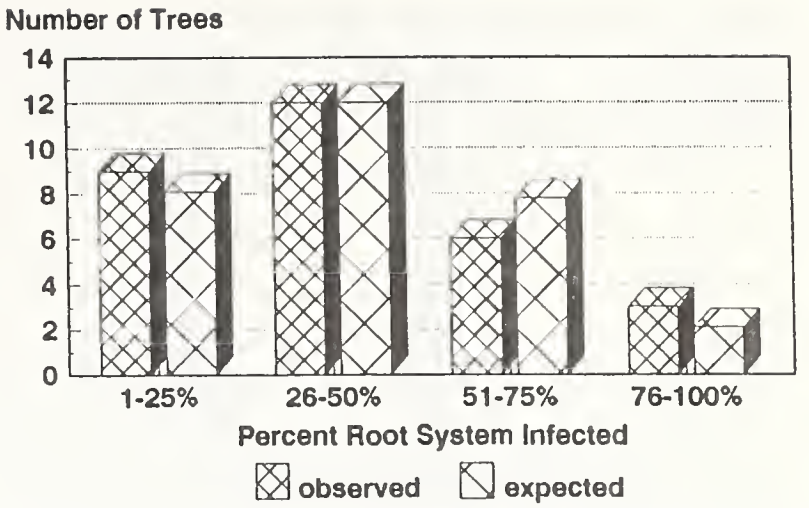


Figure 2.—The observed and expected frequency of lodgepole pine trees by infection class for truncated-binomial distribution with four classes and P = 0.495.

proportions for infected root systems, we can use table 1 to assign a proportion for a new tree. To do so we draw a number, n, at random from the uniform (0-1) distribution. This number is compared to the cumulative distribution values in table 1. If n is less than 0.27, the new tree is assigned to the first class. The proportion given the tree would be the class mid-point 0.125. If the random number, n, is greater than 0.27 but less than 0.67 (0.67 = 0.27 + 0.40), the tree is assigned to the second class. The proportion given the new tree is 0.375. If n is greater than 0.67, but less than 0.91, the tree is assigned to the third class. For n greater than 0.91, the tree is assigned to the last class. The tree has a chance of being assigned to each of the four classes, but the probability of each assignment is quite different. Less than 10 percent of the trees will be assigned to the fourth class with 0.76 to 1.00 proportion of the root system infected.

Using four mid-class values is only slightly better than assigning all the trees the same proportion. If we have confidence that the truncated-binomial distribution is a choice to represent the distribution of the proportion of root systems infected, we can obtain more resolution in the assignment of these proportions by simply increasing N. If we set N = 10 and P = 0.495 we would have 10 classes to which we could assign a new tree. The probability for each class is computed with the same distribution function as used for table 1. The new tree is assigned to any of 10 classes and is given one of the following proportions: 0.05, 0.15, 0.25, 0.34, 0.45, 0.55, 0.65, 0.75, 0.85, 0.95. The probability for assignment to each class is given in table 2 and figure 3.

Even 10 classes are not enough when dealing with a distribution with a mean of 0.10. This is the default for the Western Root Disease Model. Almost all new trees are assigned to one of the first four classes. We can again raise the value of N to 100 and accommodate all expected applications for the proportion of root system colonized.

Table 2.—Truncated-binomial distribution where P = 0.2649 and N = 10.

k	PDF(k)[1]	CDF(k)[2]
1	.1989	0.1989
2	.2983	0.4972
3	.2651	0.7625
4	.1547	0.9172
5	.0618	0.9790
6	.0171	0.9962
7	.0032	0.9995
8	.0004	0.9999
9	.0000	0.9999
10	.0000	1.0000

[1] PDF(k) is the value of the probability density function.
[2] CDF(k) is the value of the cumulative distribution function.

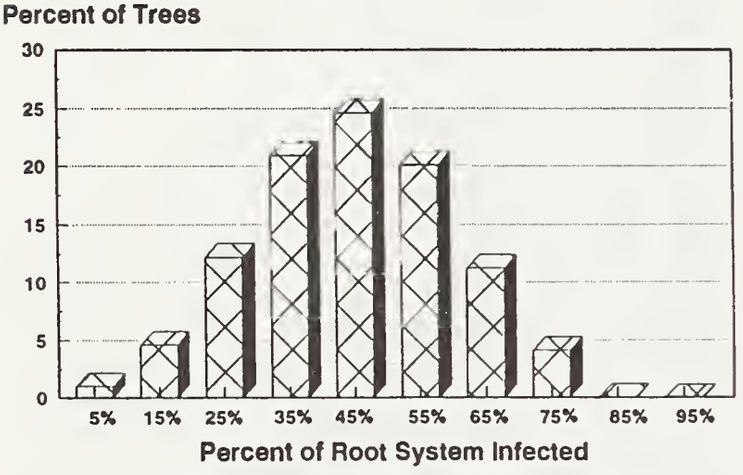


Figure 3.—The expected percentage of trees assigned to a ten-class system using the truncated-binomial with P = 0.495.

As an enhancement to the model, we added the following default proportion of tree root system colonized for trees coded as infected at inventory. "Severity codes 1, 2, and 3 are assigned the proportions 0.10, 0.65, and 0.75 respectively of the level of the root system colonized at time of death for that tree species." To implement the random assignment of proportions in the Western Root Disease Model, a FORTRAN subroutine was written. By changing the parameters, this subroutine can be used in other simulation applications. A complete listing of the subroutine is given in Appendix A.

Results and Discussion

The same stand used in the "User's Manual for Western Root Disease Model" is used to illustrate the change in the simulation model due to the addition of random proportions to represent proportion of root colonized. This stand is approximately 130 years old and situated at an elevation of 3,300 feet in a *Thuja/ Clintonia* habitat type. The stand was inventoried in 1983 and consists of grand fir (*Abies grandis*), larch (*Larix occidentalis*), red cedar (*Thuja plicata*), and Douglas-fir (*Pseudotsuga menziesii*). *Armillaria* spp. root

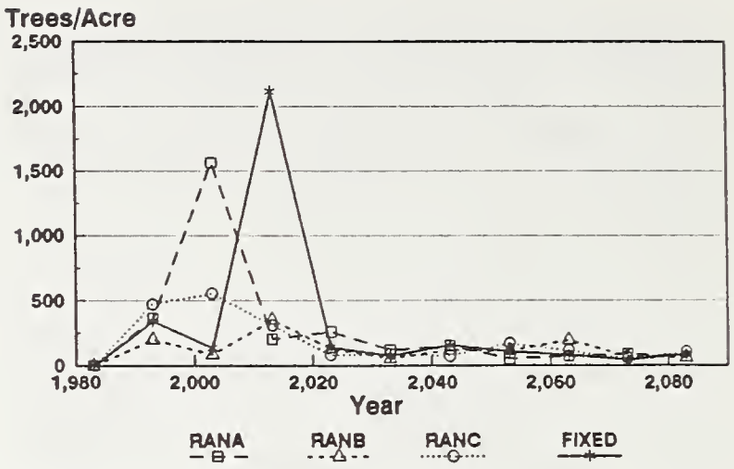


Figure 4.—Four simulations of the tree mortality within the root disease infected area of the stand; 1-3 have randomly assigned initial proportions of tree root systems infected and 4 has a fixed proportion assigned to all infected trees.

disease was detected on several sample trees during inventory. The RRTREIN keyword is used in the simulation to input this disease condition. The proportion of the root system colonized is set first as fixed (0.50) for all infected trees. In the 3 subsequent simulations, the proportion is set to 0.50, but it is distributed randomly to the sample trees, using the truncated-binomial distribution (mean 0.50, N = 10).

The use of a fixed proportion of root system colonized for all infected trees results in a peak in tree mortality after a few simulation cycles. The random assignment of proportions dampens this peak (fig. 4). The first of the random allocations produces a smaller and earlier peak in tree mortality; the other simulations do not. We believe a model that produces a sequence of possible outcomes, some of which include peaks in tree mortality, is more consistent with the true forest condition than a fixed, single-peak simulation.

The random number generator for the uniform distribution (0-1) used in this procedure is RUNIFM.F77. This routine has been tested alone and as a part of the truncated-binomial distribution. It has performed well for the limited range of values required for our application. It is public domain software.

Literature Cited

Bloomberg, W.J.; Reynolds, G. 1985. Growth loss and mortality in laminated root rot infection centers in second-growth Douglas-fir on Vancouver Island. Forest Science. 31(2): 497-508.

IMSL Inc., 1991. User's Manual FORTRAN subroutines for statistical analysis STAT/LIBRARY TM Version 2.0. September 1991: 1257-1271.

Kulhavy, David L.; Partridge, A.D.; Start, R.W. 1984. Root diseases and blister rust associated with bark beetles (*Coleoptera: Scolytidae*) in western white

pine in Idaho. Environmental Entomology. 13: 813-817.

Marsaglia, G.; Zaman, A. 1991. A new class of random number generators. The Annals of Applied Probability. 3(3): 462-480.

Parzen, E. 1967. Stochastic processes. San Francisco: Holden-Day. 324 p.

Stage, A.R.; Shaw, C.G. III; Marsden, M.A.; Byler, J.W.; Renner, D.L.; Eav, B. B.; McNamee, P.J.; Sutherland, G.D.; Webb, T.M. 1990. User's manual for the Western Root Disease Model. Gen. Tech. Rep. INT-267. Ogden, UT: U.S. Department of Agriculture, Forest Service, Intermountain Forest and Range Experiment Station. 49 p.

Tkacz, Borys M.; Schmitz, Richard F. 1986. Association of an endemic mountain pine beetle population with lodgepole pine infected by armillaria root disease in Utah. Res. Note INT-353. Ogden, UT: U.S. Department of Agriculture, Forest Service, Intermountain Forest and Range Experiment Station. 8 p.

Wykoff, William R. 1986. Supplement to the user's guide for the Stand Prognosis Model-version 5.0. Gen. Tech. Rep. INT-208. Ogden, UT: U.S. Department of Agriculture, Forest Service, Intermountain Forest and Range Experiment Station. 36 p.

Wykoff, William R.; Crookston, Nicholas L.; Stage, Albert R. 1982. User's guide to the Stand Prognosis Model. Gen. Tech. Rep. INT-133. Ogden, UT: U.S. Department of Agriculture, Forest Service, Intermountain Forest and Range Experiment Station. 112 p.

Appendix A

The computer programs written for the generation of random proportions are written in Fortran77. They have been compiled and tested on the Data General MV20000. There are five separate subroutines:

DRIVER.F77	The main routine for the test program.
RANPRP.F77	The random proportion function.
RINIT.F77	The subroutine to initialize the random number generator.
RRANN.F77	An include file needed when the subroutines are compiled.
RUNIFM.F77	The random number generator function.

There are other files needed to complete the linking of this routine to the Western Root Disease Model. For use on the Data General, a link macro is also needed.

PROGRAM DRIVER

```
C----------
C
C     MAIN PROGRAM USED TO TEST THE RANDOM PROPORTION ROUTINE
C


      REAL PROP, SEED
      CHARACTER*20 NAME

      WRITE (*,*) ' ENTER AN OUTPUT FILE NAME : '
      READ  (*,100) NAME
  100 FORMAT(A20)

      OPEN  (UNIT=8, FILE=NAME, FORM='FORMATTED',STATUS='FRESH')


      WRITE (*,*) ' ENTER A PROPORTION   : '
      READ  (*,*) PROP

      WRITE (*,*) ' ENTER A RANDOM SEED  : '
      READ  (*,*) SEED

      CALL RINIT(SEED)
```

```
      DO 200 I = 1,10
         WRITE (8,500) (RANPRP(PROP), J = 1,10)
      200 CONTINUE

      500 FORMAT (10(2X,F5.3))

         END

         REAL FUNCTION RANPRP(PROP)
C----------
C  **RANPRP  DATE OF LAST REVISION:   09/04/92
C----------
C
C  THIS FUNCTION WILL RETURN A PROPORTION BASED ON A RANDOM DRAW GIVEN
C  A MEAN PROPORTION.  IT IS BASED ON A BINOMIAL PROBABILITY
C  DENSITY FUNCTION.
C
C  CALLED BY :
C       RRINF   [ROOT DISEASE]
C
C  CALLS :
C       RUNIFM  (FUNCTION)   [ROOT DISEASE]
C
C  PARAMETERS :
C       PROP         - PROPORTION THAT IS TO BE RANDOMIZED
C
C  LOCAL VARIABLES :
C       CDF          - ARRAY THAT HOLDS THE VALUES FROM THE CUMULATIVE
C                      DISTRIBUTION FUNCTION
C       EXPROP       - THE EXPECTED PROPORTION
C       INTNUM       - NUMBER OF ITERATIONS TO RUN THE FUNCTION
C       K            - COUNTER FOR ITERATION CODE
C       L            - COUNTER FOR EXPECTED PORPORTION LOOP
C       LREV         - LOGICAL VARIABLE THAT IS SET TO .TRUE. IF PROPIN > 0.5
C                      AND 1-PROPIN IS USED FOR THE  CALCULATIONS
C       OLDPRP       - PROPIN FROM THE PREVIOUS CALL TO THIS FUNCTION
C                      (OLD PROPIN)
C       PDF          - TEMPORARY VARIABLE THAT HOLDS THE VALUE FROM THE
C                      PROBABILITY DENSITY FUNCTION
C       PROPIN       - PROPORTION THAT IS TO BE RANDOMIZED. SET TO PROP AT
```

```
C                   THE BEGINNING OF THE ROUTINE
C       RANNUM  - RANDOM NUMBER RETURNED FROM THE RANDOM NUMBER
C                   GENERATOR
C
        LOGICAL LREV
        INTEGER K, L
        REAL    RANNUM, PROP, PROPIN, OLDPRP, EXPROP
        DOUBLE PRECISION  CDF(1001), PDF
C
C       OLDPRP AND CDF WERE PUT IN A COMMON BLOCK SO THAT THEY WOULD BE
C       SAVED BETWEEN CALLS TO THIS FUNCTION
C
        COMMON  /PRPDAT/ OLDPRP, CDF
C
C       INITIALIZE L AND LREV, SET PROPIN TO PROP
C
        L = 0
        LREV   = .FALSE.
        PROPIN = PROP

C
C       INTNUM (N) IS  EQUAL TO 5 / PROPIN.
C
        INTNUM = NINT(5 / PROPIN)

        IF (INTNUM .GT. 100) INTNUM = 100
        IF (INTNUM .LT. 10)  INTNUM = 10

C
C       ADJUST PROPIN TO ACCOUNT FOR THE SHORTENING OF RANGE FROM
C       0 <= X <= 1  TO  0 < X <= 1 .
C
C       WHEN THE RANGE IS 0 < X <= 1 THE EXPECTED MEAN PROPORTION IS:
C       E = P / (1 - (1-P)**n)
C
  100 CONTINUE
        EXPROP = PROPIN / (1.0 - (1.0 - PROPIN)**INTNUM)
        IF (ABS(PROPIN - EXPROP) .GT. (1.0 / REAL(INTNUM)) .AND.
        &   L .LT. 10) THEN
```

```
        PROPIN = PROPIN - (0.5 * (PROPIN - EXPROP))
        L = L + 1
        GOTO 100
      ENDIF
C
C     CHECK TO SEE IF PROPIN > 0.5
C     IF PROPIN > 0.5 THEN SET PROPIN TO 1-PROPIN AND SET LREV TO .TRUE.
C
C     IF THE PROPORTION IS GREATER THAN 0.5 THEN USE THE CURVE FROM 0.0
C     TO 0.5 AND SET THE PROPORTION BASED ON 1-(THE MEAN PROPORTION)
C     AFTER THE RANDOM PROPORTION IS CALCULATED THEN THE PROPORTION IS
C     REVERSED AGAIN PROPIN = 1-(RANDOM PROPORTION CALCULATED)
C
      IF (PROPIN .GT. 0.5) THEN
          PROPIN = 1.0 - PROPIN
          LREV = .TRUE.
      ENDIF

C
C     THIS SECTION OF CODE ONLY NEEDS TO BE EXECUTED IF THE PROPORTION
C     READ IN HAS CHANGED SINCE THE LAST TIME THIS FUNCTION WAS CALLED
C
      IF (PROPIN .NE. OLDPRP) THEN
C
C         SET OLDPRP TO PROPIN TO SAVE PROPIN
C
      OLDPRP = PROPIN

C
C     SET PDF AND CDF FOR FIRST ITERATION
C
      PDF = (1.0 - PROPIN)**INTNUM
      CDF(1) = PDF

C
C     CALCULATE PDF FOR ALL ITERATIONS AND SET CDF
C
C     PDF(K|P,N) = PDF(K-1|P,N) * (P/(1-P)) * (N-K+1) / K
C
```

```
      DO 200 K = 1,INTNUM
         PDF = PDF * (PROPIN / (1.0-PROPIN) *
     &            REAL(INTNUM - K + 1)) / REAL(K)
C
C        ADJUST CDF VALUE TO ACCOUNT FOR THE TRUNCATED RANGE
C        0 < X <= 1
C
      CDF(K+1) = CDF(K) + (PDF / (1.0 - CDF(1)))
  200 CONTINUE
      ENDIF

C
C     LOOP TO GET RANDOM NUMBER THAT IS GREATER THAN ZERO
C
  300 RANNUM = RUNIFM()
      IF (RANNUM .EQ. 0.0) THEN
         GOTO 300
      ENDIF

C
C     INITIALIZE RANPRP AND K
C
      RANPRP = 0.7 * (1.0 / REAL(INTNUM))
      K = 1

C
C     LOOP THROUGH THE CURVE CDF(K+1) UNTIL THE RANDOM NUMBER FITS
C     THE CURVE
C
  400 CONTINUE
      IF (RANNUM .GE. CDF(K+1) .AND. K .LE. INTNUM) THEN
         RANPRP = REAL(K+1) / REAL(INTNUM)
         K = K + 1
         GOTO 400
      ENDIF

C
C     IF PROPIN WAS > 0.5 THEN RESET RANPRP TO 1.0-RANPRP
C     BECAUSE PROPIN WAS SET TO 1.0-PROPIN
```

```
C
      IF (LREV) THEN
         RANPRP = 1.0 - RANPRP
      ENDIF

      RETURN
      END
CODE SEGMENT RRANN
C----------
C     **RRANN DATE OF LAST REVISION:  09:00:00 11/06/89
C----------
         DOUBLE PRECISION S0, S1

         COMMON /RRANN/ S0, S1, SS
C
C        S0   --HOLDS THE CURRENT SEED FOR THE RANDOM NUMBER GENERATOR.
C        S1   --HOLDS INTERMEDIATE VALUE IN RANDOM NUMBER GENERATOR.
C                THIS VALUE BECOMES THE NEXT SEED.
C        SS   --USED IN THE INITIALIZATION OF THE RANDOM NUMBER GENERATOR.
C
C----------END SEGMENT
         REAL FUNCTION RUNIFM()
C----------
C     **RUNIFM DATE OF LAST REVISION:  11:30:00 11/06/89
C----------
C
C     THIS FUNCTION RETURNS A UNIFORM RANDOM NUMBER TO THE ROOT
C     DISEASE MODEL CALLING ROUTINE.
C
C     THIS RANDOM NUMBER GENERATED WAS MODIFIED FROM THE ALGORITHM
C     FOUND IN THE IMSL LIBRARY VOL 1 EDITION 4 TO 5,
C     DEC. 1, 1975, AND CAN BE FOUND IN THE FOLLOWING REFERENCES:
C
C     LEWIS, P.A.W., GOODMAN, A.S., AND MILLER, J.M. PSUEDO-RANDOM
C     NUMBER GENERATOR FOR THE SYSTEM/360, IBM SYSTEMS JOURNAL, NO. 2,
C     1969.
C
C     LEARMONTH, G.P. AND LEWIS, P.A.W., NAVAL POSTGRADUATE SCHOOL
C     RANDOM NUMBER GENERATOR PACKAGE LLRANDOM, NPS55LW73061A, NAVAL
```

```
C       POSTGRADUATE SCHOOL, MONTEREY, CALIFORNIA, JUNE, 1973.
C
C       LEARMONTH, G.P., AND LEWIS, P.A.W., STATISTICAL TESTS OF SOME
C       WIDELY USED AND RECENTLY PROPOSED UNIFORM RANDOM NUMBER
C       GENERATORS. NPS55LW73111A, NAVAL POSTGRADUATE SCHOOL, MONTEREY
C       CALIFORNIA, NOV. 1973.
C
C       THE CODE WAS WRITTEN BY N.L. CROOKSTON, FORESTRY SCIENCES LAB,
C       OCT 1982, FROM THE ALGORITHM PUBLISHED IN THE IMSL MANUAL AND
C       TESTED BY COMPARING THE FIRST 10000 DRAWS FROM THIS VERSION AND
C       THE GENERATOR 'GGUBS' IN THE 1981 EDITION OF IMSL.
C
C       CALLS   :
C           NONE
C
C       COMMON BLOCK VARIABLES USED :
C           S0    - (RRANN)      INPUT/OUTPUT
C           S1    - (RRANN)      OUTPUT
C
COMMONS
C
C
            INCLUDE 'RRANN.F77'
C
C
COMMONS
C
            S1 = DMOD(16807D0*S0,2147483647D0)
            RUNIFM = S1 / 2147483648D0
            S0 = S1

            RETURN
            END

            SUBROUTINE RINIT(SSEED)
C----------
C       **RINIT  DATE OF LAST REVISION:  11:30:00 11/06/89
C----------
C       THIS SUBROUTINE INITIALIZED THE RANDOM NUMBER GENERATOR FOR THE
```

```
C     ROOT DISEASE MODEL.
C
C     CALLS:
C         NONE
C
C     PARAMETERS:
C         SSEED -  SEED VALUE FOR THE ROOT DISEASE RANDOM NUMBER
C                  GENERATOR
C
C     LOCAL VARIABLES :
C         ISEED  -  INTEGER VALUE OF SSEED.  SEED VALUE FOR THE ROOT DISEASE
C                  RANDOM NUMBER GENERATOR.
C
C     COMMON VARIABLES USED :
C         SS - (RRANN)        OUTPUT
C         S0 - (RRANN)        OUTPUT
C
COMMON
C
C
      INCLUDE 'RRANN.F77'
C
C
COMMONS
C
      ISEED = INT(SSEED)
      IF (MOD(ISEED,2) .EQ. 0) ISEED = ISEED + 1
      SS = FLOAT (ISEED)
      S0 = SS

      RETURN
      END
```

USDA policy prohibits discrimination because of race, color, national origin, sex, age, religion, or handicapping condition. Any person who believes he or she has been discriminated against in any USDA-related activity should immediately contact the Secretary of Agriculture, Washington, DC 20250.